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 "dynamic mutations" because of changes in the number of repeat units inherited from generation to generation (Koshy, *et al.*, *Brain Pathol*, 7:927-42 (1997)). Although these repeats are highly polymorphic, their number usually does not exceed 40 repeats in normal individuals (Online Mendelian Inheritance in Man, OMIM (TM). Johns Hopkins University, Baltimore, MD. MIM Number: 603279; jlewis :7/14/1999; World Wide Web URL: ncbi.nlm.nih.gov/omim; Koshy, *et al.* (1997)).--

[Delete the paragraph spanning lines 1-20 of page 11, and insert the following]

therefor:

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 -- The term "homologous recombination" refers to the exchange of DNA fragments between two DNA molecules or chromatids at the site of homologous nucleotide sequences, i.e., those sequences preferably having at least about 70 percent sequence identity, typically at least about 85 percent identity, and preferably at least about 90 percent identity, alternatively, at least about 95-98 percent identity. Homology and/or percent identity can be determined using a "BLASTN" algorithm, such as BLAST (Basic Local Alignment Search Tool) 2.0, available on-line at, ncbi.nlm.nih.gov:80/BLAST/, (Basic, Advanced or PSI) and as described in any of Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." *J. Mol. Biol.* 215:403-410. (Medline); Gish, W. & States, D.J. (1993) "Identification of protein coding regions by database similarity search." *Nature Genet.* 3:266-272. (Medline); Madden, T.L., Tatusov, R.L. & Zhang, J. (1996) "Applications of network BLAST server" *Meth. Enzymol.* 266:131-141. (Medline); Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman,

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D.J. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs." Nucleic Acids Res. 25:3389-3402. (Medline); and Zhang, J. & Madden, T.L. (1997) "PowerBLAST: A new network BLAST application for interactive or automated sequence analysis and annotation." Genome Res. 7:649-656. (Medline) It is understood that homologous sequences can accommodate insertions, deletions and substitutions in the nucleotide sequence. Thus, linear sequences of nucleotides can be essentially identical even if some of the nucleotide residues do not precisely correspond or align.--

IN THE CLAIMS

Amend the claims as follows:

Cancel claims 1-65, without prejudice.

Add the following claims:

66. (new) A cell comprising a disruption in a target DNA sequence encoding a TRP, wherein said target gene sequence is T243 or a naturally occurring allelic variation thereof.

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67. (new) A cell comprising a disruption in a target DNA sequence encoding a TRP, wherein said target gene sequence is T243.

68. (new) A cell comprising a disruption in a target DNA sequence encoding a TRP, wherein the target DNA sequence comprises SEQ ID NO:47.

69. (new) A cell comprising a disruption in a target DNA sequence encoding a TRP, wherein the target DNA sequence comprises SEQ ID NO:45 and SEQ ID NO:46.